(1) GENERAL INFORMATION:

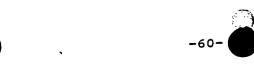
- APPLICANT: Reed, John
- TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
- (iii) NUMBER OF SEQUENCES: 23
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Gray, Cary, Ames & Frye
 - (B) STREET: 401 B Street, Suite 1700
 - (C) CITY: San Diego
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: \Q2101-4297
 - (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING \SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NOMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:

 - (A) NAME: Brotman, Harris F. (B) REGISTRATION NUMBER: 35461
 - (C) REFERENCE/DOCKET NUMBER: P0041US0
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 699-3 €30
 - (B) TELEFAX: (619) 236-1048
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iv) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCTTCCTAC CGCGTGCGAC

(2)	INFORMATION FOR SEQ ID NO:2:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(iv) ANTI-SENSE: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CTTT	TCCTCT GGGAAGGATG GCGCACGCTG GGAGA	35
(2)	INFORMATION FOR SEQ ID NO:3:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(iv) ANTI-SENSE: YES	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CCTC	CGACCC ATCCACGTAG	20
(2)	INFORMATION FOR SEQ ID NO:4:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(iv) ANTI-SENSE: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	

ACGGGGTACG GAGGCTGGGT AGGTGCATCT GGT



(2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GTTGACGTCC TACGGAAACA
(2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: CCCCCAACTG CAGGATGCCT TTGTGGAACT GTACGG
(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GGGAAGGATG GCGCACGCTG

(2) INFORMATION FOR SEQ ID NO:8:

20

36

	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iv)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:8:	
CGCC	STGCG.	AC CCTCTTG	17
(2)	INFO	RMATION FOR SEQ ID NO:9:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iv)	ANTI-SENSE: YES	
TAC	•	SEQUENCE DESCRIPTION: SEQ ID NO:9:	17
		RMATION FOR SEQ ID NO:10:	
		SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(iv)	ANTI-SENSE: YES	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:10:	
TCC	FACCG	CG TGCGACC	17
(2)	INFO	RMATION FOR SEQ ID NO:11:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
CCTTCCTACC GCGTGCG	17
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: GACCCTTCCT ACCGCGT	17
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	17
GGAGACCCTT CCTACCG	
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	·- · · ,

(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	15
GCGGCGGCAG CGCGG	10
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	15
CGGCGGGCG ACGGA	
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	16
CGGGAGCGCG GCGGGC	
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
TCTCCCAGCG TGCGCCAT	18
(2) INFORMATION FOR SEQ ID NO:18:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
TGCACTCACG CTCGGCCT	18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

(XI) St	SQUENCE DESC	EXIFITON. DI	. <u>.</u>	•		
GCGCCCGCCC	CTCCGCGCCG	CCTGCCCGCC	CGCCCGCCGC	GCTCCCGCCC	GCCGCTCTCC	60
GTGGCCCCGC	CGCGCTGCCG	CCGCCGCCGC	TGCCAGCGAA	GGTGCCGGGG	CTCCGGGCCC	120
TCCCTGCCGG	CGGCCGTCAG	CGCTCGGAGC	GAACTGCGCG	ACGGGAGGTC	CGGGAGGCGA	180
CCGTAGTCGC	GCCGCCGCGC	AGGACCAGGA	GGAGGAGAAA	GGGTGCGCAG	CCCGGAGGCG	240
GGGTGCGCCG	GTGGGGTGCA	GCGGAAGAGG	GGGTCCAGGG	GGGAGAACTT	CGTAGCAGTC	300
		GAAAAAATAA				360
		GCGCGGGCTT				420
		CAGCTTTTCG				480
		GTCCCCGGCT				540
		TCCCGTGGAT				600
		GAAGGGGAAA				660
		CGCCGCCGCT				720
		TTGACATTTC				780
		CCCTCTCCCC				840
-						900
		CTGAAGATTG				960
		GACAGAGGAT				1020
		ATGTAACTTT				
		ATTTCCAGGC				1080
		TTTCACTCAG				1140
		TTAACCTTTC				1200
		GTGCCTCATG				1260
AATTTCCTGC	GTCTCATGCC	AAGAGGGAAA	CACCAGAATC	AAGTGTTCCG	CGTGATTGAA	1320





CAACTCCCAA	TACTGGCTCT	GTCTGAGTAA	GAAACAGAAT	CCTCTGGAAC	TTGAGGAAGT	3060
GAACATTTCG	GTGACTTCCG	ATCAGGAAGG	CTAGAGTTAC	CCAGAGCATC	AGGCCGCCAC	3120.
AAGTGCCTGC	TTTTAGGAGA	CCGAAGTCCG	CAGAACCTAC	CTGTGTCCCA	GCTTGGAGGC	3180
CTGGTCCTGG	AACTGAGCCG	GGCCCTCACT	GGCCTCCTCC	AGGGATGATC	AACAGGGTAG	3240
TGTGGTCTCC	GAATGTCTGG	AAGCTGATGG	ATGGAGCTCA	GAATTCCACT	GTCAAGAAAG	3300
AGCAGTAGAG	GGGTGTGGCT	GGGCCTGTCA	CCCTGGGGCC	CTCCAGGTAG	GCCCGTTTTC	3360
ACGTGGAGCA	TAGGAGCCAC	GACCCTTCTT	AAGACATGTA	TCACTGTAGA	GGGAAGGAAC	3420
AGAGGCCCTG	GGCCTTCCTA	TCAGAAGGAC	ATGGTGAAGG	CTGGGAACGT	GAGGAGAGGC	3480
AATGGCCACG	GCCCATTTTG	GCTGTAGCAC	ATGGCACGTT	GGCTGTGTGG	CCTTGGCCAC	3540
CTGTGAGTTT	AAAGCAAGGC	TTTAAATGAC	TTTGGAGAGG	GTCACAAATC	CTAAAAGAAG	3600
CATTGAAGTG	AGGTGTCATG	GATTAATTGA	CCCCTGTCTA	TGGAATTACA	TGTAAAACAT	3660
TATCTTGTCA	CTGTAGTTTG	GTTTTATTTG	AAAACCTGAC	AAAAAAAAAG	TTCCAGGTGT	3720
GGAATATGGG	GGTTATCTGT	ACATCCTGGG	GCATTAAAAA	AAAATCAATG	GTGGGGAACT	3780
ATAAAGAAGT	AACAAAAGAA	GTGACATCTT	CAGCAAATAA	ACTAGGAAAT	TTTTTTTTCT	3840
TCCAGTTTAG	AATCAGCCTT	GAAACATTGA	TGGAATAACT	CTGTGGCATT	ATTGCATTAT	3900
ATACCATTTA	TCTGTATTAA	CTTTGGAATG	TACTCTGTTC	AATGTTTAAT	GCTGTGGTTG	3960
ATATTTCGAA	AGCTGCTTTA	ААААААТАСА	TGCATCTCAG	CGTTTTTTTG	TTTTTAATTG	4020
	TGGCCTATAC				•	4080
	GATTCTTCAA					4140
	AACCTGGATG					4200
	GTCAACAGAA				•	4260
				•	GTATTCAGGA	4320
					GATGGCGAAT	4380
					CGTGGCCTGT	4440
					TCTCATGGCT	4500
					AGCAGGAAAC	4560
					CAGACCTTTG	4620
AATGATTCT	ATITTTAAGO	TATTATAAAA :	TTTATGAAAG	GTTTACATTG	TCAAAGTGAT	4680





GAATATGGAA T	ATCCAATCC	TGTGCTGCTA	TCCTGCCAAA	ATCATTTTAA	TGGAGTCAGT	4740
TTGCAGTATG C	TCCACGTGG	TAAGATCCTC	CAAGCTGCTT	TAGAAGTAAC	AATGAAGAAC	4800
GTGGACGTTT I	AAATATAAT	GCCTGTTTTG	TCTTTTGTTG	TTGTTCAAAC	GGGATTCACA	4860
GAGTATTTGA A						4920
CTTTTGCTGT G	GGGTTTTGT	TACCTGGTTT	TAATAACAGT	AAATGTGCCC	AGCCTCTTGG	4980
CCCCAGAACT G	TACAGTATT	GTGGCTGCAC	TTGCTCTAAG	AGTAGTTGAT	GTTGCATTTT	5040
CCTTATTGTT A	AAAACATGT	TAGAAGCAAT	GAATGTATAT	AAAAGC		5086



(2) INFORMATION FOR SEQ ID NO:20:

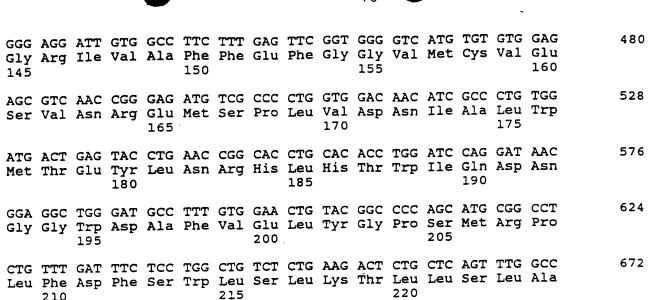
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 717 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..717
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.20.																	
ATG Met 1	GCG Ala	CAC His	GCT Ala	GGG Gly 5	AGA Arg	ACG Thr	GGG Gly	TAC Tyr	GAC Asp 10	AAC Asn	CGG Arg	GAG Glu	ATA Ile	GTG Val 15	ATG Met		48
AAG Lys	TAC Tyr	ATC Ile	CAT His 20	TAT Tyr	AAG Lys	CTG Leu	TCG Ser	CAG Gln 25	AGG Arg	GGC Gly	TAC Tyr	GAG Glu	TGG Trp 30	GAT Asp	GCG Ala		96
GGA Gly	GAT Asp	GTG Val	GGC Gly	GCC Ala	GCG Ala	CCC Pro	CCG Pro 40	GGG Gly	GCC Ala	GCC Ala	CCC Pro	GCA Ala 45	CCG Pro	GGC Gly	ATC Ile	1	44
TTC Phe	TCC Ser 50	TCC Ser	CAG Gln	CCC Pro	GGG Gly	CAC His 55	ACG Thr	CCC Pro	CAT His	CCA Pro	GCC Ala 60	GCA Ala	TCC Ser	CGC	GAC Asp	1	.92
CCG Pro 65		GCC Ala	AGG Arg	ACC Thr	TCG Ser 70	CCG Pro	CTG Leu	CAG Gln	ACC Thr	CCG Pro 75	GCT Ala	GCC Ala	CCC Pro	GGC Gly	GCC Ala 80	2	40
	GCG Ala	GGG Gly	CCT Pro	GCG Ala 85	CTC Leu	AGC Ser	CCG Pro	GTG Val	CCA Pro 90		GTG Val	GTC Val	CAC His	CTG Leu 95	GCC Ala	2	288
CTC Leu	CGC Arg	CAA Gin	GCC Ala	GIA	GAC Asp	GAC Asp	TTC Phe	TCC Ser 105	n- 9	CGC	TAC	CGC Arg	GGC Gly 110	GAC Asp	TTC Phe	:	336
GCC Ala	GAG Glu	ATG Met	Ser	AGC Ser	CAG Gln	CTG Leu	CAC His	ישבי	ACG Thr	CCC Pro	TTC Phe	ACC Thr	GCG	CGG Arg	GGA Gly		384
CGC Arg	TTT Phe	GCC Ala		GTG Val	GTG Val	GAG Glu 135	GIU	CTC Lev	TTC Phe	AGG Arg	GAC Asp 140	-	GTC Val	AAC Asn	TGG Trp		432

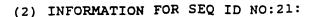
235

717



CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT CTG AGC CAC AAG

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys



(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe 105 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp 135 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala

220

.



Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys 225 230 235

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

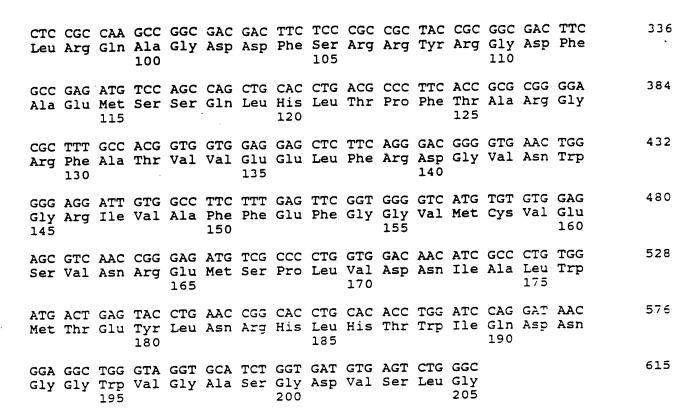
- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

				 			AAC Asn	 	 	 48
							GGC Gly			96
							GCC Ala			144
	-	-		 	-	_	CCA Pro			192
							CCG Pro 75			240
							CCT Pro			288



(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala 20 25 30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
35 40 45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp 50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala 65 70 75 80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala Ser Pro Val Pro Pro Val Val His Leu Ala Ser Arg Arg Tyr Arg Gly Asp Phe 105 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Pro Pro Thr Ala Arg Gly Arg Phe 130 Ala Thr Val Val Glu Glu Leu Pro Arg Asp Gly Val Asn Trp 130 Arg Ile Val Ala Pro Pro Glu Pro Gly Gly Val Met Cys Val Glu 160 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asp Asn Ile Ala Leu Trp 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn 180 185 190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly 195 200 205